primary amino acid sequence similar to that of decarbamylase by utilizing a stereostructure of the decarbamylase crystal according to claim 1, or a stereostructure of decarbamylase according to claim 14 or 16.

REMARKS

The above-identified application is a U.S. National Stage application under 35 U.S.C. §371 of copending PCT international application PCT/JP00/05901, filed 30 August 2000.

Claims 5-7 and 18-19 have been amended to provide correct antecedent basis; claims 5, 7, 19-20, 22, 24, 26, and 31-32 have been amended without prejudice to delete excessive multiple dependent claims; and claims 24 and 26 have also been amended to correct improper claim formats. No new matter has been added by these amendments. Applicant respectfully requests entry of this Preliminary Amendment which is submitted in the format required under 37 C.F.R. § 1.121 together with a marked-up version of the replacement paragraphs/sections. Applicant respectfully requests entry of this Preliminary Amendment.

Accordingly upon entry of the Preliminary Amendment, claims 1-35, as amended, will be pending and under examination in the subject application.

Respectfully submitted,

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Version with markings to show changes made:

5. (Amended) Decarbamylase crystal [Crystal] according to claim[s] 1[-4], wherein the crystal contains at least one or more heavy metal atoms per decarbamylase molecule.

6. (Amended) Decarbamylase crystal [Crystal] according to claim 5, wherein the heavy metal atom is any of mercury, gold, platinum, lead, iridium, osmium, and uranium.

7. (Amended) Frozen decarbamylase crystal, prepared by freezing the decarbamylase crystal according to [any one of] claim[s] 1[-6] in liquid nitrogen.

18. (Amended) An enzyme molecule according to claim 17, wherein in a reaction, the D-N-carbamoyl-α-amino acid can interact with amino acids corresponding to Lys at position 126, His at position 143, Glu at position 145, Arg at position 174, Arg at position 175, and Thr at position 197 of SEQ ID NO.: 1 or 2 at the active site cavity, or an active fragment thereof.

19. (Amended) An enzyme molecule according to claim 17 [or 18], wherein amino acids corresponding to Glu at position 46, Glu at position 145, and Cys at position 171 of SEQ ID NO.: 1 or 2 have a hydrogen bond via a water molecule at the active site cavity, or an active fragment thereof.

20. (Amended) An enzyme molecule according to [any one of] claim[s] [16-19] 17, wherein the D-N-carbamoyl-α-amino acid is selected from the group consisting of D-N-carbamoyl-phenylglycine, D-N-carbamoyl-parahydroxyphenylglycine, D-N-carbamoyl-phenylalanine, D-N-carbamoyl-valine, D-N-carbamoyl-alanine, D-N-carbamoyl-cysteine, D-N-carbamoyl-aspartic acid, D-N-carbamoyl-glutamic acid, D-N-carbamoyl-glycine, D-N-carbamoyl-histidine, D-N-carbamoyl-isoleucine, D-N-carbamoyl-lysine, D-N-carbamoyl-leucine, D-N-carbamoyl-methionine, D-N-carbamoyl-asparagine, D-N-carbamoyl-proline, D-N-carbamoyl-glutamine, D-N-carbamoyl-arginine, D-N-carbamoyl-serine, D-N-carbamoyl-threonine, D-N-carbamoyl-tryptophan, and D-N-carbamoyl-tyrosine, or an active fragment thereof.

22. (Amended) A method for designing decarbamylase mutants, comprising the step of designing the decarbamylase mutants having a physical property and/or a function modified based on [a] the stereostructure of decarbamylase according to [any one of] claim[s] 14[,] or 16[, and 21].

24. (Amended) A method [according to claim 23] for designing decarbamylase mutants, comprising the steps of: preparing a crystal of an enzyme having decarbamylase activity; determining a stereostructure of the crystal by subjecting the crystal to X-ray crystallography; and designing the decarbamylase mutants having an improved physical property and/or function based on the determined stereostructure, wherein the stereostructure is a stereostructure of decarbamylase according to [any

one of] claim[s] 14[,] or 16[, and 21].

26. (Amended) ~~A method [according to claim 25]~~ for designing decarbamylase mutants, comprising the steps of: preparing a crystal of an enzyme having decarbamylase activity; determining a stereostructure of the crystal by subjecting the crystal to X-ray crystallography; designing the decarbamylase mutants having an improved physical property and/or function based on the determined stereostructure; and producing the decarbamylase mutants, wherein the stereostructure is a stereostructure of decarbamylase according to [any one of] claim[s] 14[,] or 16[, and 21].

31. (Amended) A decarbamylase mutant obtained with a production method according to [any one of] claim[s 25-30] 26.

32. (Amended) A method for modifying a polypeptide or protein enzyme having a primary amino acid sequence similar to that of decarbamylase by utilizing a stereostructure of the decarbamylase crystal according to [any one of] claim[s] 1[-7], or a stereostructure of decarbamylase according to [any one of] claim[s] 14[,] or 16[, and 21].